

1/8

Sequence Listing

<110> Tatsuji, Seki and Kazuhito, Fujiyama
<120> Methods for production of glycoproteins
5 having human-type sugar chains
<130> J198080401
<150> JP P1998-350584
<151> 1998-12-09
<160> 6
10 <170> PatentIn Ver. 2.0

<210> 1
<211> 31
<212> DNA
15 <213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer hGT-5Eco
<400> 1
aaagaattcg cgatgccagg cgcgcgtccc t 31
20
<210> 2
<211> 28
<212> DNA
<213> Artificial Sequence
25 <220>
<223> Description of Artificial Sequence: primer hGT-2Sal
<400> 2
tcgatcgcaa aaccatgigc agcigatg 28
30
<210> 3
<211> 29
<212> DNA
<213> Artificial Sequence

2/8

<220>
 <223> Description of Artificial Sequence: primer hGT-7Spe
 <400> 3
 acgggactcc tcaggggcga tgaatcataa 29

5

<210> 4
 <211> 27
 <212> DNA
 <213> Artificial Sequence

10

<220>
 <223> Description of Artificial Sequence: primer hGT-6Spe
 <400> 4
 aagactagtg ggccccaatgc tgattga 27

15

<210> 5
 <211> 1158
 <212> DNA
 <213> Homo sapiens

20

<220>
 <221> CDS
 <222> (1)..(1155)
 <400> 5
 atg cca ggc gcg tcc cta cag cgg gcc tgc cgc ctg ctc gtc gcc gtc 48
 Met Pro Gly Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val

25

1 5 10 15
 tgc gct ctg cac ctt ggc gtc acc ctc gtt tac tac ctg gct ggc cgc 96
 Cys Ala Leu His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg
 20 25 30

30

gac ctg agc cgc ctg ccc caa ctg gtc gga gtc tcc aca ccg ctg cag 144
 Asp Leu Ser Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln
 35 40 45

3/8

ggc ggc tgc aac agt gcc gcc gcc atc ggg cag tcc tcc ggg gag ctc 192
 Gly Gly Ser Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu
 50 55 60

5

cgg acc gga ggg gcc cgg ccg ccg cct cct cta ggc gcc tcc tcc cag 240
 Arg Thr Gly Gly Ala Arg Pro Pro Pro Pro Leu Gly Ala Ser Ser Gln
 65 70 75 80

10

ccg cgc ccg ggt ggc gac tcc agc cca gtc gtg gat tct ggc cct ggc 288
 Pro Arg Pro Gly Gly Asp Ser Ser Pro Val Val Asp Ser Gly Pro Gly
 85 90 95

15

ccc gct agc aac ttg acc tgc gtc cca gtg ccc cac acc acc gca ctg 336
 Pro Ala Ser Asn Leu Thr Ser Val Pro Val Pro His Thr Thr Ala Leu
 100 105 110

20

tgc ctg ccc gcc tgc cct gag gag tcc ccg cta cta gtg ggc ccc atg 384
 Ser Leu Pro Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly Pro Met
 115 120 125

25

ctg att gag ttt aac atg cct gtg gac ctg gag ctc gtg gca aag cag 432
 Leu Ile Glu Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala Lys Gln
 130 135 140

30

aac cca aat gtg aag atg ggc gcc cgc tat gcc ccc agg gac tgc gtc 480
 Asn Pro Asn Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp Cys Val
 145 150 155 160

tct cct cac aag gtg gcc atc atc att cca ttc cgc aac cgg cag gag 528
 Ser Pro His Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg Gln Glu
 165 170 175

4/8

cac ctc aag tac tgg cta tat tat ttg cac cca gtc ctg cag cgc cag 576
 His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln Arg Gln
 180 185 190

5 cag ctg gac tat ggc atc tat gtt atc aac cag gcg gga gac acf ata 624
 Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp Thr Ile
 195 200 205

10 ttc aat cgt gct aag ctc ctc aat gtt ggc ttt caa gaa gcc ttg aag 672
 Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Gln Gln Ala Leu Lys
 210 215 220

15 gac tat gac tac acc tgc ttt gtg ttt agt gac gtg gac ctc att cca 720
 Asp Tyr Asp Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu Ile Pro
 225 230 235 240

atg aat gac cat aat gcg tac agg tgt ttt tca cag cca cgg cac att 768
 Met Asn Asp His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg His Ile
 245 250 255

20 tcc gtt gca atg gat aag ttt gga ttc agc cta cct tat gtt cag tat 816
 Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr
 260 265 270

25 ttt gga ggt gtc tct gct cta agt aaa caa cag ttt cta acc atc aat 864
 Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn
 275 280 285

30 gga ttt cct aat aat tat tgg ggc tgg gga gga gaa gat gat gac att 912
 Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Gln Asp Asp Asp Ile
 290 295 300

ttt aac aga tta gtt ttt aga ggc atg tct ata tct cgc cca aat gct 960

5/8

Phe Asn Arg Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala
 305 310 315 320

5 gig gtc ggg agg tgt cgc atg atc cgc cac tca aga gac aag aaa aat 1008
 Val Val Gly Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn
 325 330 335

10 gaa ccc aat cct cag agg ttt gac cga att gca cac aca aag gag aca 1056
 Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr
 340 345 350

15 atg ctc tct gat ggt ttg aac tca ctc acc tac cag gtg ctg gat gta 1104
 Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val
 355 360 365

20 cag aga tac cca ttg tat acc caa atc aca gtg gac atc ggg aca ccg 1152
 Gln Arg Tyr Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly Thr Pro
 370 375 380

25 agc tag 1158
 Ser
 385

30 <210> 6
 <211> 385
 <212> PRT
 <213> Homo sapiens
 <400> 6
 Met Pro Gly Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val
 1 5 10 15

Cys Ala Leu His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg
 20 25 30

6/8

	Asp	Leu	Ser	Arg	Leu	Pro	Gln	Leu	Val	Gly	Val	Ser	Thr	Pro	Leu	Gln	
				35					40						45		
5	Gly	Gly	Ser	Asn	Ser	Ala	Ala	Ala	Ile	Gly	Gln	Ser	Ser	Gly	Gln	Leu	
				50					55						60		
	Arg	Thr	Gly	Gly	Ala	Arg	Pro	Pro	Pro	Pro	Leu	Gly	Ala	Ser	Ser	Gln	
				65					70					75			80
10	Pro	Arg	Pro	Gly	Gly	Asp	Ser	Ser	Pro	Val	Val	Asp	Ser	Gly	Pro	Gly	
						85						90				95	
	Pro	Ala	Ser	Asn	Leu	Thr	Ser	Val	Pro	Val	Pro	His	Thr	Thr	Ala	Leu	
15					100					105						110	
	Ser	Leu	Pro	Ala	Cys	Pro	Glu	Glu	Ser	Pro	Leu	Leu	Val	Gly	Pro	Met	
					115					120						125	
20	Leu	Ile	Glu	Phe	Asn	Met	Pro	Val	Asp	Leu	Glu	Leu	Val	Ala	Lys	Gln	
					130					135						140	
	Asn	Pro	Asn	Val	Lys	Met	Gly	Gly	Arg	Tyr	Ala	Pro	Arg	Asp	Cys	Val	
					145					150				155		160	
25	Ser	Pro	His	Lys	Val	Ala	Ile	Ile	Ile	Pro	Phe	Arg	Asn	Arg	Gln	Glu	
						165					170					175	
	His	Leu	Lys	Tyr	Trp	Leu	Tyr	Tyr	Leu	His	Pro	Val	Leu	Gln	Arg	Gln	
30						180					185					190	
	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	Asn	Gln	Ala	Gly	Asp	Thr	Ile	
						195					200					205	

7/8

Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Gln Glu Ala Leu Lys
210 215 220

5 Asp Tyr Asp Tyr Thr Cys Phe Val Phe Ser Asp Val Asp Leu Ile Pro
225 230 235 240

Met Asn Asp His Asn Ala Tyr Arg Cys Phe Ser Gln Pro Arg His Ile
245 250 255

10 Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr
260 265 270

Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn
15 275 280 285

Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Ile
290 295 300

20 Phe Asn Arg Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala
305 310 315 320

Val Val Gly Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn
325 330 335

25 Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr
340 345 350

Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val
30 355 360 365

Gln Arg Tyr Pro Leu Tyr Thr Gln Ile Thr Val Asp Ile Gly Thr Pro
370 375 380

WO 00/34490

09/857651

PCT/JP99/06881

8/8

Ser

385